



0590
1018

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/901,484
Source: OLPE
Date Processed by STIC: 10/23/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker will also be used to check sequence listings in Computer Readable form.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/20/484

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 3rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 10/23/2001

PATENT APPLICATION: US/09/901,484

TIME: 16:31:00

Input Set : A:\GEN-T111XC3D2-seqlist.txt

Output Set: N:\CRF3\10232001\I901484.raw

3 <110> APPLICANT: Cohen, Daniel
 4 Blumenfeld, Marta
 5 Ilya, Chumakov
 6 Bougueleret, Lydie
 8 <120> TITLE OF INVENTION: PROSTATE CANCER GENE
 10 <130> FILE REFERENCE: GEN-T111XC3D2
 12 <140> CURRENT APPLICATION NUMBER: 09/901,484
 13 <141> CURRENT FILING DATE: 2001-07-09
 15 <150> PRIOR APPLICATION NUMBER: 08/996,306
 16 <151> PRIOR FILING DATE: 1997-12-22
 18 <150> PRIOR APPLICATION NUMBER: 60/099,658
 19 <151> PRIOR FILING DATE: 1998-09-09
 21 <150> PRIOR APPLICATION NUMBER: 09/218,207
 22 <151> PRIOR FILING DATE: 1998-12-22
 24 <150> PRIOR APPLICATION NUMBER: 09/338,907
 25 <151> PRIOR FILING DATE: 1999-06-23
 27 <150> PRIOR APPLICATION NUMBER: 09/853,526
 28 <151> PRIOR FILING DATE: 2001-05-11
 30 <160> NUMBER OF SEQ ID NOS: 578
 32 <170> SOFTWARE: Patent.pm

ERRORED SEQUENCES

2650 <210> SEQ ID NO: 69
 2651 <211> LENGTH: 5226
 2652 <212> TYPE: DNA
 2653 <213> ORGANISM: Homo sapiens
 2655 <400> SEQUENCE: 69

P4

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2657				Met Arg Tyr Leu Leu Pro Ser Val	
2658				1 5	
2659	gtg ctc ctg ggc acg gcg ccc acc tac gtg ttg gcc tgg ggg gtc tgg				102
2660	Val Leu Leu Gly Thr Ala Pro Thr Tyr Val Leu Ala Trp Gly Val Trp				
2661	10	15	20		
2662	cgg ctg ctc tcc gcc ttc ctg ccc gcc cgc ttc tac caa gcg ctg gac				150
2663	Arg Leu Leu Ser Ala Phe Leu Pro Ala Arg Phe Tyr Gln Ala Leu Asp				
2664	25	30	35	40	
2665	gac cgg ctc tac tgc gtc tac caa agc atg gtg ctc ttc ttc ttc gag				198
2666	Asp Arg Leu Tyr Cys Val Tyr Gln Ser Met Val Leu Phe Phe Phe Glu				
2667	45	50	55		
2673	75	80	85		

RAW SEQUENCE LISTING

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Output Set: N:\CRF3\10232001\I901484.raw

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2676      90                      95                      100
2677 cgc tac gtg ctg aaa gaa ggg tta aaa tgg ctg cca ttg tat ggg tgt      390
2678 Arg Tyr Val Leu Lys Glu Gly Leu Lys Trp Leu Pro Leu Tyr Gly Cys
2679 105                      110                      115                      120
2680 tac ttt gct cag cat gga gga atc tat gta aag cgc agt gcc aaa ttt      438
2681 Tyr Phe Ala Gln His Gly Gly Ile Tyr Val Lys Arg Ser Ala Lys Phe
2682                      125                      130                      135
2683 aac gag aaa gag atg cga aac aag ttg cag agc tac gtg gac gca gga      486
2684 Asn Glu Lys Glu Met Arg Asn Lys Leu Gln Ser Tyr Val Asp Ala Gly
2685                      140                      145                      150
2686 act cca atg tat ctt gtg att ttt cca gaa ggt aca agg tat aat cca      534
2687 Thr Pro Met Tyr Leu Val Ile Phe Pro Glu Gly Thr Arg Tyr Asn Pro
2688                      155                      160                      165
2689 gag caa aca aaa gtc ctt tca gct agt cag gca ttt gct gcc caa cgt      582
2690 Glu Gln Thr Lys Val Leu Ser Ala Ser Gln Ala Phe Ala Ala Gln Arg
2691                      170                      175                      180
2692 ggc ctt gca gta tta aaa cat gtg cta aca cca cga ata aag gca act      630
2693 Gly Leu Ala Val Leu Lys His Val Leu Thr Pro Arg Ile Lys Ala Thr
2694 185                      190                      195                      200
2695 cac gtt gct ttt gat tgc atg aag aat tat tta gat gca att tat gat      678
2696 His Val Ala Phe Asp Cys Met Lys Asn Tyr Leu Asp Ala Ile Tyr Asp
2697                      205                      210                      215
2698 gtt acg gtg gtt tat gaa ggg aaa gac gat gga ggg tag cgaagagagt      727
2699 Val Thr Val Val Tyr Glu Gly Lys Asp Asp Gly Gly *
2700                      220                      225
2701 caccgaccat gacggaatTT ctctgcaaaG aatgtccaaa aattcatatt cacattgacT      787
2702 gtatcgacaa aaaagatgtc ccagaagaac aagaacatat gagaagatgg ctgcatgaac      847
2703 gtttcgaaat caaagataag atgcttatag aattttatga gtcaccagat ccagaaagaa      907
2704 gaaaaagatt tcttgggaaa agtggttaatt ccaaattaag tatcaagaag actttaccat      967
2705 caatgttgat ctttaagtggT ttgactgcag gcatgcttat gaccgatgct ggaagggaagc      1027
2706 tgtatgtgaa cacttgata tatggaaccc tacttggtcg cctgtgggtt actattaaag      1087
2707 catagacaag tagctgtctc cagacagtgg gatgtgctac attgtctatt tttggcggtc      1147
2708 qcacatgaca tcaaatTgtt tcttgaatTT attaaggagt gtaaataaaG ccttggtgat      1207
2709 tgaagattgg ataataqaat ttgtgaagaa agctgatatg caatggtctt gggcaaacat      1267
2710 acctggttgt acaacttttag catcggggct gctggaaggg taaaagctaa atqgaqTtTc      1327
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2712 attttgcaag tcagatggct qcatttttga gcattaattt gcagcgtatt tcactttttc      1447
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2715 gtattttagga agtgtccagga tgttccaaagg aaagggtaaa aagtgttccat ggggaaaaaag      1627
2716 ctctgttttag cacatgattt tattgtattg cgttatttagc tgattttact catttttatat      1687
2717 ttqcaaaaata aattttctaT atttattgaa attgcttaat ttgcacaccc tqtacacaca      1747
2718 gaaaatggta taaaatatga gaacgaagtt taaaattgtg actctgatTc attatagcag      1807
2719 aacttttaaat ttcccaqctt ttTgaagatt taaqctacgc tattagtaact tccctttgtc      1867

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RAW SEQUENCE LISTING

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Output Set: N:\CRF3\10232001\I901484.raw

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2725	gaagaaatgc	agagccagcc	tgtgctgccc	actttcagag	ttgaactctt	taagcccttg	2227
2726	tgagtgggct	tcaccagcta	ctgcagaggg	attttgcatt	tgtctgtgtc	aagaagtcca	2287
2727	ccttctcaag	ccagtgaagt	acagacttaa	ttcgatcatg	ctgaacgaat	ttgtttattt	2347
2728	cccattaggt	ttagtggagc	tacacattaa	tatgtatcgc	cttagagcaa	gagctgtgtt	2407
2729	ccaggaaacca	gatcacgatt	tttagccatg	gaacaatata	tcccatggga	gaagaccttt	2467
2730	cagtgtgaac	tgttctattt	ttgtgttata	atttaaactt	cgatttcttc	atagtccctt	2527
2731	aagttgacat	ttctgcttac	tgtactgga	tttttgcctg	agaaatatat	cagtggccca	2587
2732	cattaaacat	accagttgga	tcagtataag	caaaatgaaa	gaaataatga	ttaagggaaa	2647
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2734	tctttgaaga	gtcggtgtgt	gtgaattggt	ttgtgtacat	tagaatgtat	gcacacatcc	2767
2735	atggacactc	aggatatagt	tggcctaata	atcgggcat	gggtaaaact	tatgaaaatt	2827
2736	tctcatgct	gaattgtaat	ttctctttac	ctgtaaagta	aaatttagat	caattccatg	2887
2737	tctttgttaa	gtacagggat	ttaatatatt	ttgaatataa	tgggtatgtt	ctaaatttga	2947
2738	actttgagag	gcaatactgt	tgggaattatg	tggattctaa	ctcattttta	caaggtagcc	3007
2739	tgacctgcac	aagatcactt	gaatgttagg	tttcatagaa	ctatacta	cttctcacia	3067
2740	aaggctctata	aaatacagtc	gttgaaaaaa	attttgtatc	aaaatgtttg	gaaaattaga	3127
2741	agcttctcct	taacctgtat	tgatactgac	ttgaattatt	ttctaaaatt	aagagccgta	3187
2742	tacctacctg	taagtctttt	cacatatcat	ttaaactttt	gtttgtatta	ttactgattt	3247
2743	acagcttagt	tattaatttt	tctttataag	aatgccgtcg	atgtgcacgc	ttttatgttt	3307
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2758	agacacacag	taactcccaq	atatgtacca	caaaaatgt	gaaaagagag	agaaatgtct	4207
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2760	tttgttttta	gtagtgttta	gattgaagat	tgagtgaagt	atlttcttgg	caqatattcc	4327
2761	gtatctgggt	gaaagctaca	atgcaatgtc	gttgtagtgt	tgcattggct	gctttataaa	4387
2762	caagattttt	tctccctcct	tttgggccag	ttttcattac	gagttaactca	cactttttga	4447
2763	ttaaagaact	tgaattacg	ttatcactta	gtataattga	cattatatag	agactatgta	4507
2764	acatgcaatc	attagaatca	aaattagtag	tttgggtcaa	atattttacaa	cattcacata	4567
2765	cttgctcaaat	attcatgtaa	ttactgaat	ttaaaacctt	caactattat	gaagtgtctg	4627
2766	tctgtacaat	cgtataattta	ctcagtttag	agtagctaca	actcttcgat	actatcatca	4687
2767	atattttgaca	tcttttccaa	tttgtgtatg	aaaagtaaat	ctatttctgt	agcaactggg	4747
2768	gagtcataata	tgaaggtcaa	gacatatacc	ttgttattat	aatatqtata	ctataataat	4807

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/901,484

DATE: 10/23/2001

TIME: 16:31:01

Input Set : A:\GEN-T111XC3D2-seqlist.txt

Output Set: N:\CRF3\10232001\I901484.raw

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2774 tgtctcttta tggatatttc agaataaagt ctgacttggtg tttttgagat tattggtgcc 5167
E--> 2775 tcattaattc agcaataaag gaaaatatgc atttcaaaaa naaaaaaaaa aaaaaaaaaa 5226
16099 <210> SEQ ID NO: 578
16100 <211> LENGTH: 19
16101 <212> TYPE: DNA
16102 <213> ORGANISM: Homo Sapiens
16104 <220> FEATURE:
16105 <221> NAME/KEY: misc_feature
16106 <222> LOCATION: 1..19
16107 <223> OTHER INFORMATION: potential microsequencing oligo for 99-222-109.mis2
16109 <400> SEQUENCE: 578
16110 ctgaagaaat tcatatcgt 19
E--> 16112 (283)

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see also Gen Bank Summary Sheet

delete

Post

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/901,484

DATE: 10/23/2001

TIME: 16:31:04

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Output Set: N:\CRF3\10232001\I901484.raw

L:453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
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L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:1323 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:1419 M:283 W: Missing Blank Line separator, <400> field identifier
L:1737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:2162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:2775 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:69
L:2782 M:283 W: Missing Blank Line separator, <400> field identifier
L:2819 M:283 W: Missing Blank Line separator, <400> field identifier
L:2908 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:72
L:2911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:2964 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
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L:3110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73
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L:3630 M:283 W: Missing Blank Line separator, <400> field identifier
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/901,484

DATE: 10/23/2001

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Output Set: N:\CRF3\10232001\I901484.raw

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L:8038 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8053 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
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L:8320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8321 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:183
L:8741 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:184
L:16112 M:254 E: No. of Bases conflict, LENGTH:Input:283 Counted:19 SEQ:578